

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: January 31, 2005, 09:45:33 ; Search time 2226.25 Seconds
 (without alignments) 8496.727 Million cell updates/sec

Title: US-09-996-630A-11_COPY_1_400
 Perfect score: 400

Sequence: 1 gtctaaaggtgtaaagacc.....ccaaaattgtatccccag 400

Scoring table: IDENTITY_NUC
 Gapext 1.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:
 1: gb_ba: *
 2: gb_htg: *
 3: gb_in: *
 4: gb_om: *
 5: gb_ov: *
 6: gb_pt: *
 7: gb_ph: *
 8: gb_pl: *
 9: gb_pr: *
 10: gb_ro: *
 11: gb_sts: *
 12: gb_sy: *
 13: gb_un: *
 14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ALIGNMENTS			
Result No.	Score	Query Match Length	DB ID	Description	ORIGIN
1	400	100.0	4165	AX329586 Sequence COT22611 Sequence AX166529 Sequence AX6422970 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 AC121264 AC120394 AC106612 Rattus no BC075868 Danio rer BC060922 Danio rer	RESULT 1 AX329586 LOCUS Sequence 95 from Patent WO014629. 4165 bp DNA linear DEFINITION Sequence 95 from Patent WO014629. ACCESSION AX329586.1 GI:18102564 VERSION AX329586.1 KEYWORDS SOURCE ORGANISM Homo sapiens (human) Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo sapiens REFERENCE AUTHORS Young, P.E., Augustus M. Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Sppet, D.R. and Weaver, Z. TITLE Cancer gene determination and therapeutic screening using signature gene sets JOURNAL Patent: WO 0194629-A 95 13-DEC-2001; Avalon Pharmaceuticals (US) FEATURES source 1. .4165 /organism="Homo sapiens" /mol-type="unassigned DNA" /db_xref="TAXON:9606"
2	398.4	99.6	2193	6 C072611 Sequence AX166529 Sequence AX6422970 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
3	398.4	99.6	2298	6 AX6422970 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
4	398.4	99.6	4772	6 AX6422970 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
5	398.4	99.6	4882	9 HUMKRAQ Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
6	398.4	99.6	5519	9 AF226044 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
7	396.8	99.2	5140	9 BC071567 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
8	323.8	81.0	4708	10 AF387809 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
9	322.2	80.5	3101	10 BC020189 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
10	322.2	80.5	3101	10 BC020189 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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12	212	53.0	143034	9 AC10484 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
13	212	53.0	186485	2 AC138808 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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15	171.8	43.0	194261	10 AC120394 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
16	171.8	43.0	206641	10 AC120394 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
17	168.2	42.0	252055	2 AC106612 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
18	137.2	34.3	1253	5 BC075868 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
19	130.8	32.7	2834	5 BC060922 Sequence D41636 Human mRNA AR226044 Homo sapi BC071567 Homo sapi AF387809 Mus muscu X99383 R. norvegicus BC020189 Mus muscu AC118087 Rattus no AC10484 Homo sapi AC138808 Homo sapi AC143769 Macaca mulatta AC121264 Mus musculus AC120394 Mus musculus AC106612 Rattus norvegicus BC075868 Danio rer BC060922 Danio rer	Query Match Score 400; DB 6; Length 4165; Best Local Similarity 100.0%; Pred. No. 2.7e-108; Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
C0722611
LOCUS C0722611 2193 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 8545 from Patent WO02068579.
ACCESSION C0722611.1 GI:42263468
VERSION C0722611.1
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1. Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
PATENT: WO 02068579-A 8545 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
source 1. .21.93
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<ab_xref="taxon:9606"

ORIGIN
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Best Local Similarity 99.8%; Pred. No. 7.9e-108;
Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTCTAAAGAGTGTAAAGACCTTAATACCGGAGCTACAGAGAGATCCAGAGAAGGC
Db 609 GTCTAAAGAGTGTAAAGACCTTAATACCGGAGCTACAGAGAGATCCAGAGAAGGC
Qy 61 TCTTTGAAGGATGAAATCATCTTGCTTCAGGGACTGGAGATGCCAACAGAGAGGC
Db 774 TCTTTGAAGGATGAAATCATCTTGCTTCAGGGACTGGAGATGCCAACAGAGAAGGC
Qy 121 AAGTATAACATCCCCCTGTCATACAAATTCTGGAGAGGGCACACGCCAT
Db 834 AAGTATAACATCCCCCTGTCATACAAATTCTGGAGAGGGCACACGCCAT
Qy 181 CATTCAACGGCATGGTGTGGGACATAGCGATCGAGGACCCATAGAGCCCTGGA
Db 894 CATTCAACGGCATGGTGTGGGACATAGCGATCGAGGACCCATAGAGCCCTGGA
Qy 241 AACCAACAGGTTAACCATATCACACGCCATACTCTCTGTGGTGTGGAGATCTCGAG
Db 954 AACCAACAGGTTAACCATATCACACGCCATACTCTCTGTGGTGTGGAGATCTCGAG
Qy 61 TCCTTAGAGAGATGAAATCATCTTGCTTCAGGGAGTCCAGCTAC
Db 669 TCCTTAGAGAGATGAAATCATCTTGCTTCAGGGAGTCCAGCTAC
Qy 121 AAAGTATAACATCCCCCTGTCATACAAATCTCTGGAGAGGGACACAGCAT
Db 729 AAAGTATAACATCCCCCTGTCATACAAATCTCTGGAGAGGGACACAGCAT
Qy 181 CATTCAACGGCATGGTGTGGGACATAGCGATCGAGGACCCATAGAGCCCTGGA
Db 789 CATTCAACGGCATGGTGTGGGACATAGCGATCGAGGACCCATAGAGCCCTGGA
Qy 241 AACCAACAGGTTAACCATATCACACGCCATACTCTCTGTGGTGTGGAGATCTCGAG
Db 849 AACCAACAGGTTAACCATATCACACGCCATACTCTCTGTGGTGTGGAGATCTCGAG
Qy 301 AGAAAGCAAGAGAAATACAGACCATGATCGAGGCCAGCHATATCAAGGCCA
Db 360 AGAAAGCAAGAGAAATACAGACCATGATCGAGGCCAGCHATATCAAGGCCA
Qy 909 AGAAAGCAAGAGAAATACAGACCATGATCGAGGCCAGCHATATCAAGGCCA
Db 361 GTTTAGGCACTATGCCAACCAAATGTGATGCCAG 400
Db 969 GTTTAGGCACTATGCCAACCAAATGTGATGCCAG 1008

RESULT 3
AX166529
LOCUS AX166529 2298 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 20 from Patent WO0138503.
ACCESSION AX166529
VERSION AX166529.1 GI:14546874
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1. Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanan,S.S., Martinez,R., Flanagan,P. and Clary,D.S.
AUTHORS Novel human protein kinases and protein kinase-like enzymes
TITLE
JOURNAL Patent: WO 0138503-A 20 31-MAY-2001;
Patent: US 6498036-B1 20 31-MAY-2001;
Sugen, Inc. (US)
Location/Qualifiers
1. .2298
<organism="Homo sapiens"
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<db_xref="taxon:9606"

ORIGIN
Query Match 99.6%; Score 398.4; DB 6; Length 2298;
Best Local Similarity 99.8%; Pred. No. 7.9e-108;
Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTCTAAAGAGTGTAAAGACCTTAATACCGGAGCTACAGAGAGATCCAGAGAAGGC
Db 714 GTCTAAAGAGTGTAAAGACCTTAATACCGGAGCTACAGAGAGATCCAGAGAAGGC
Qy 61 TCTTTGAAGGATGAAATCATCTTGCTTCAGGGACTGGAGATGCCAACAGAGAGGC
Db 773 TCTTTGAAGGATGAAATCATCTTGCTTCAGGGACTGGAGATGCCAACAGAGAAGGC
Qy 121 AAGTATAACATCCCCCTGTCATACAAATTCTGGAGAGGGCACACGCCAT
Db 833 AAGTATAACATCCCCCTGTCATACAAATTCTGGAGAGGGCACACGCCAT
Qy 181 CATTCAACGGCATGGTGTGGGACATAGCGATCGAGGACCCATAGAGCCCTGGA
Db 893 CATTCAACGGCATGGTGTGGGACATAGCGATCGAGGACCCATAGAGCCCTGGA
Qy 241 AACCAACAGGTTAACCATATCACACGCCATACTCTCTGTGGTGTGGAGATCTCGAG
Db 953 AACCAACAGGTTAACCATATCACACGCCATACTCTCTGTGGTGTGGAGATCTCGAG
Qy 61 TCCTTAGAGAGATGAAATCATCTTGCTTCAGGGAGTCCAGCTAC
Db 728 TCCTTAGAGAGATGAAATCATCTTGCTTCAGGGAGTCCAGCTAC
Qy 121 AAAGTATAACATCCCCCTGTCATACAAATCTCTGGAGAGGGACACAGCAT
Db 1014 AAAGTATAACATCCCCCTGTCATACAAATCTCTGGAGAGGGACACAGCAT
Qy 361 GTTTAGGCACTATGCCAACCAAATGTGATGCCAG 400
Db 1073 GTTTAGGCACTATGCCAACCAAATGTGATGCCAG 1113
Qy 909 AGAAAGCAAGAGAAATACAGACCATGATCGAGGCCAGCHATATCAAGGCCA
Db 968 AGAAAGCAAGAGAAATACAGACCATGATCGAGGCCAGCHATATCAAGGCCA
Qy 301 AGAAAGCAAGAGAAATACAGACCATGATCGAGGCCAGCHATATCAAGGCCA
Db 360 AGAAAGCAAGAGAAATACAGACCATGATCGAGGCCAGCHATATCAAGGCCA
Qy 909 AGAAAGCAAGAGAAATACAGACCATGATCGAGGCCAGCHATATCAAGGCCA
Db 361 GTTTAGGCACTATGCCAACCAAATGTGATGCCAG 400
Db 969 GTTTAGGCACTATGCCAACCAAATGTGATGCCAG 1008

RESULT 4
AX642970
LOCUS AX642970 4772 bp DNA linear PAT 24-FEB-2003
DEFINITION Sequence 47 from Patent WO01096547.
ACCESSION AX642970
VERSION AX642970.1 GI:28550119
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1. Yee,H., Lal,P., Bandman,O., Borowsky,M., Au-Young,J., Lu,Y., Gandhi,A.R., Tribouley,C.M., Walla,N., Yao,M.G., Lu,D.A., Greenwald,S.R., Rankumar,J., Griffin,J.A., Kearney,L., Burford,N.,

FEATURES		COMMENT	On May 9, 2002 this sequence version replaced 91:598957.
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/note="Incyte ID No: 063497CBI"		/db_xref="taxon:9606"	
Location/Qualifiers		/clone="had124081"	
/organism="Homo Sapiens"		/sex="male"	
/mol_type="unassigned DNA"		/cell_line="KG-1"	
/note="Incyte ID No: 063497CBI"		/cell_type="myeloblast"	
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Location/Qualifiers		/note="This sequence was obtained by subcloning of the DNA	
Query Match	99.6%	fragments derived from two cDNA clones (1 - 1013 was	
Best Local Similarity	99.8%	derived from a RT-PCR product (Lung) and 1014 - 4882 was	
Matches	399;	derived from ha01240).	
Conservative	0;	1. 4882	
Mismatches	1;	/gene="KIAA0095"	
Indels	0;	/codon_start=2	
Gaps	0;	/protein_id="BA007744.2"	
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Qy		/translation="SMAGFRGDDKIGLYLDLWLGHRFAVVKLARHYPTGEKVA	
Db		VRVIIKTKLDTLATEFLQEVRCMLVQHENVIRKJEDVQTQKLTILEBGDGIMF	
Qy		DYIMKHEBEGIUNEDLAKYFQIWHVSYCHLHVWRDPLVYFPEKFQCGVLPDP	
Db	1030	ANDSEITLMINDCKTIVPSVSKKECDLITRMLQDQPKRRASLEIENHPWLOQVDFP	
Qy		PATKKNPLVSYKNSBEERINITORNWLIDADDAIVELETYRNHTAYFILIA	
Db		ERILBKQKEIOTOMPSKPTAPDILPQDPLTAPLHSATVPODPLSP	
Qy		ARRADEVLNGRSKQGICDSARKKDDIFELAGALSTVPPASIKPTASGRKCLPFRVEDE	
Db		EDEBEDKPKMSLSTOVLRLRKPSVNRLTRSKVPAVLNQFPEGGSDKDRPMDENLPW	
Qy		KLSRIQNLNLSPGTHYMRKSSRSQSSSSTSDDSESRQPKLSSRQGKTFWPH	
Db	1150	RDRSSGPSPGSBEGD3EGQSKESNSAQSGVDKASPSMNAAGGESPSSSGGNTNTSGT	
Qy		RRCAPSNMOLASAGENLVEISLUSLICGQSORHGSKTYIDRONGLSPSSVVKYQ	
Db		RSKTRWNCISSTSGNAGKOFPVANGIKPFSKUDMHADTTTELERIKSKNUKVNQLPCEKT	
Db	1210	ISVN1QRNPKEGLLACASSPACCHV1"	
Qy		ORIGIN	
Db	361	Query Match	
Qy		Best Local Similarity	
Db	361	99.6%	
Qy		Score	
Db	361	398.4	
Qy		DB:	
Db	361	9	
Qy		Length	
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Qy		ORIGIN	
Db	1270	Query Match	
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Db	1270	99.6%	
Qy		Score	
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Qy		DB:	
Db	1270	9	
Qy		Length	
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Db	61	99.6%	
Qy		Score	
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Qy		DB:	
Db	61	9	
Qy		Length	
Db	61	4882	
Qy		ORIGIN	
Db	778	Query Match	
Qy		Best Local Similarity	
Db	778	99.6%	
Qy		Score	
Db	778	398.4	
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Db	778	9	
Qy		Length	
Db	778	4882	
Qy		ORIGIN	
Db	121	Query Match	
Qy		Best Local Similarity	
Db	121	99.6%	
Qy		Score	
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Db	838	99.6%	
Qy		Score	
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Qy		Length	
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Qy		ORIGIN	
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Db	958	99.6%	
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Db	958	9	
Qy		Length	
Db	958	4882	
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Qy		Best Local Similarity	
Db	241	99.6%	
Qy		Score	
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Qy		Length	
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Qy		Score	
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Qy		DB:	
Db	361	9	
Qy		Length	
Db	361	4882	
Qy		ORIGIN	
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Qy		Best Local Similarity	
Db	1018	99.6%	
Qy		Score	
Db	1018	398.4	
Qy		DB:	
Db	1018	9	
Qy		Length	
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Qy		ORIGIN	
Db	1018	Query Match	
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Qy		Score	
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Db	1018	4882	
Qy		ORIGIN	
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Qy		Score	
Db	1017	398.4	
Qy		DB:	
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Qy		DB:	
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Qy		ORIGIN	
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Qy		Length	
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 Qy 121 AAGTATACTATCCCTGTGTCATCAAATCTCGAGAGGAGCAACAGAT 180
 Db 982 CAAGTATACTATCCCTGTGTCATCAAAGAACCTCTCGAGGAAGCAGCAT 1041
 Qy 181 CATTAGGGCATGGTGTGGGACATAGGGATGGAGAGCATTGAGAAGCCCTGAG 240
 Db 1042 CATCCAGGATGGTGTGGGACATGGGAGACCATGCGGAGAGCAGCATGGAGAAGCCCTGAG 1101
 Qy 241 AACCAACAGGTATAACCATACAGGCACACTTCTCTGCTGTAAGAAAGATCTCTGAG 300
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 Qy 301 AGAAACAGGAGAAAGAACAGACAGATGCGAGGAGATATCAAGGCCA 360
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RESULT 9
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 LOCUS DEFINITION R.norvegicus mRNA for SNF1-related kinase.
 ACCESSION X89383
 VERSION X89383.1 GI:1213223
 KEYWORDS SNF1-related kinase; snrk gene.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 Rattus norvegicus
 Rattus.
 REFERENCE 1 Becker,W., Heukelbach,J., Kentrup,H. and Joost,H.G.
 AUTHORS Molecular cloning and characterization of a novel mammalian protein
 kinase harboring a homology domain that defines a subfamily of
 serine/threonine kinase
 TITLE Bur. J. Biochem. 235 (3), 736-743 (1996)
 JOURNAL MEDLINE 9614553
 PUBLMED 8654423
 REFERENCE 2 (bases 1 to 3004)
 AUTHORS Heukelbach,J.
 TITLE Direct Submission
 JOURNAL Submitted (03-JUL-1995) J. Heukelbach, Institut fuer Pharmakologie
 und Toxik., der RWTH Aachen, Wendlingweg 2, D-52057 Aachen, FRG
 FEATURES Source

RESULT 10
 BC020189 BC020189 3101 bp mRNA linear ROD 29-JUN-2004
 LOCUS DEFINITION Mus musculus SNF related kinase, mRNA (cDNA clone MGC:28970
 IMAGE:4482701), complete cds.
 ACCESSION BC020189
 VERSION BC020189.1 GI:18843575
 KEYWORDS MGC.
 SOURCE MUS
 ORGANISM Mus musculus (house mouse)
 Mus musculus
 Buiaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciuromathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 3101)
 AUTHORS Strausberg,R.L., Feingold,B.A., Groube,L.H., Derge,J.G., Wagner,L., Shemmen,C.M., Schuler,G.D., Altchuk,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Blat,N.K., Hopkins,R.P., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.M., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carminci,P., Prange,C., Rana,S.S., Loqueline,N.A., Peters,G.J., Abramson,R.D., Mulahay,S.J., Boscak,S.A., McBewan,P.J., McKernan,K.J., Malek,J.A., Gunnarathne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Munay,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahney,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,T., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,B.D.,

Query Match 80.5%; Score 322.2; DB 10; Length 3004;
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 Matches 351; Conservative 0; MisMatches 48; Indels 0; Gaps 0;
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 Db 863 GCTGCGGGGAGGGACTCTACAGGGATGCGAGGAGTGGACCCCTAC 922
 Qy 61 TCTTTGAGAGGATGAAATCATCTTGGCTCAGGGAGTGACCCTAC 120
 Db 923 CTCTCTGGAGAGGATGAAAGGCCACCTTGGCTCAGGGAGTGGACCCCTAC 982

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 Qy 241 AACCAACAGGTATAACCATACAGGCACATCTGAGAGGAGTGGACCTTGCG 300
 Db 1103 AACCAACAGGTACAACCATACGGCAGCTACTCTTACTTGCTGAGGCG 1162
 Qy 361 GTTGTAGGAGCTATGCCAACCAAATGTGATGACCCCA 399
 Db 1223 GTTGTAGGAGCTATGCCAACCAAATGTGATGACCCCA 1260

Qy 121 AAAGTATAACATCCCTGGTCATCAAATCTCGAGAGGAGCAACGGCAT 180
 Db 983 CAGTATAACATCCCTGGTCATCAAAGACCTCTCGAGAGGAGCAACGGCAT 1042
 Qy 181 CATTAGGGCATGGTGTGGGACATAGGGATGGAGATGAGCCCTGAG 240
 Db 1043 CATTAGGGCATGGTGTGGGACATAGGGATGGAGATGAGCCCTGAG 1102
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 Db 1103 AACCAACAGGTACAACCATACGGCAGCTACTCTTACTTGCTGAGGCG 1162
 Qy 361 GTTGTAGGAGCTATGCCAACCAAATGTGATGACCCCA 399
 Db 1223 GTTGTAGGAGCTATGCCAACCAAATGTGATGACCCCA 1260

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Qy 121 AAAGTATAACATCCCTGGTCATCAAATCTCGAGAGGAGCAACGGCAT 180
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 Db 1103 AACCAACAGGTACAACCATACGGCAGCTACTCTTACTTGCTGAGGCG 1162
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 Db 1103 AACCAACAGGTACAACCATACGGCAGCTACTCTTACTTGCTGAGGCG 1162
 Qy 361 GTTGTAGGAGCTATGCCAACCAAATGTGATGACCCCA 399
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 Db 1103 AACCAACAGGTACAACCATACGGCAGCTACTCTTACTTGCTGAGGCG 1162
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 Qy 361 GTTGTAGGAGCTATGCCAACCAAATGTGATGACCCCA 399
 Db 1223 GTT

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html)

Milosavljevic,A., Miner,G., Minn,E., Montemayor,J., Moore,S.,
 Morgan,M., Morris,S., Munidas,M., Murphy,M., Nair,L.,
 Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
 Nwakelume,O., Okwuonu,G., Olarunpagonao,A., Paul,S., Parks,K.,
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 Pusa,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reich,R.,
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 Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
 Sanders,W., Saverry,G., Scheer,S., Scott,G., Shatman,S., Shen,H.,
 Shetty,J., Savart-Beynon,A., Sisson,I., Sitter,C.D., Smajs,D.,
 Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
 Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
 Taylor,T., Thomas,N., Thomas,S., Tingye,A., Trojano,Z., Usmani,K.,
 Vajas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
 Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., Whitley,F.,
 Williams,G., Willson,R., Wlcek,R., Woodin,H., Worley,K.,
 Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
 Yu,D., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
 Niederauer,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
 Weinstock,G., and Gibbs,R.A.

Direct Submission
 Unpublished
 2 (bases 1 to 249901)
 Worley,K.C.
 Direct Submission
 Submitted (13-APR-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 248901)

Rat Genome Sequencing Consortium.

Direct Submission
 Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Nov 19, 2002 this sequence version replaced gi:23194785.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly ('contig-scaffold'). Within each contig scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

----- Project Information
 Center project name: GRPK
 Center clone name: CH230-3.8M5
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 230944 bases at least Q40
 Consensus quality: 233870 bases at least Q30
 Consensus quality: 235397 bases at least Q20
 Estimated insert size: 239916; sum-of-contigs estimation
 Quality coverage: 5x in 200 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 74533: contig of 74533 bp in length
 * 74534 74533: gap of unknown length
 * 74534 23493: contig of 159860 bp in length
 * 23494 23453: gap of unknown length
 * 23494 248901: contig of 14308 bp in length.
FEATURES
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 Location/Qualifiers
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 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /db Xref="taxon:10116"
 /clone="CH230-38MS"
 15891..158713
 /note="clone_boundary
 clone_end:T7
 site:
 end_sequence:BR2811.10"

ORIGIN

Query Match 68.8%; Score 275; DB 2; Length 248901;
 Best Local Similarity 85.2%; Pred. No. 6.9e-71;
 Matches 323; Conservative 0; Mismatches 45; Indels 11; Gaps 1;

FEATURES source

Query Match Best Local Similarity 93.0%; Score 212; DB 9; Length 186485;
Matches 221; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 19 CCTPAATTACAGGGATGTCACAGAGAGAATGCCAAGAGAGGGCTCTTAGAGAGATGTA 78
Db 63915 CCTAATCACAGGGATGTCACAGAGAGATCCAAAGAGAGGGCTCTTAGAGAGATGTA 63974

Qy 79 AATCATCCTTGCTTGGAGACTGGACCCCTCACCGCTAACAGCAATTCAGGGATGGCTCT 138
Db 63975 AAATCATCCTTGCTTGGAGACTGGACCCCTCACCGCTAACAGCAATTCAGGGATGGCTCT 64034

Qy 139 TGTGTCTATAGAAATCTCTGGAGAGGAACAACAGCAATTCAGGGATGGCTCT 198
Db 64035 TGTGTCTATAGAAATCTCTGGAGAGGAACAACAGCAATTCAGGGATGGCTCT 64094

Qy 199 TGGGACATAGGGATGAGGACGCCATGTGAGTACGTCATGGCTCAATGCCGTCACT 254
Db 64095 TGGGACATAGGGATGAGGACGCCATGTGAGTACGTCATGGCTCAATGCCGTCACT 64150

ORIGIN

RESULT 13

AC138808/c AC138808 186485 bp DNA linear HTG 21-JAN-2003
LOCUS Homo sapiens chromosome 5 clone RP11-1026L22, WORKING DRAFT
DEFINITION Homo sapiens chromosome 5 clone RP11-1026L22, WORKING DRAFT
SEQUENCE, 5 unordered pieces.

ACCESSION AC138808
VERSION AC138808.1
KEYWORDS HTG; HTGS PHASEI; HTGS_DRAFT; HTGS_ACTIVEFFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 186485)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 186485)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1688774
Center clone name: RPCI-11_1026L22

FEATURES source

Query Match Best Local Similarity 93.6%; Score 212; DB 9; Length 143034;
Matches 221; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 19 CCTPAATTACAGGGATGTCACAGAGAGAATGCCAAGAGAGGGCTCTTAGAGAGATGTA 78
Db 63915 CCTAATCACAGGGATGTCACAGAGAGATCCAAAGAGAGGGCTCTTAGAGAGATGTA 63974

Qy 79 AATCATCCTTGCTTGGAGACTGGACCCCTCACCGCTAACAGCAATTCAGGGATGGCTCT 138
Db 63975 AAATCATCCTTGCTTGGAGACTGGACCCCTCACCGCTAACAGCAATTCAGGGATGGCTCT 64034

Qy 139 TGTGTCTATAGAAATCTCTGGAGAGGAACAACAGCAATTCAGGGATGGCTCT 198
Db 64035 TGTGTCTATAGAAATCTCTGGAGAGGAACAACAGCAATTCAGGGATGGCTCT 64094

Qy 199 TGGGACATAGGGATGAGGACGCCATGTGAGTACGTCATGGCTCAATGCCGTCACT 254
Db 64095 TGGGACATAGGGATGAGGACGCCATGTGAGTACGTCATGGCTCAATGCCGTCACT 64150

ORIGIN

Query Match Best Local Similarity 93.0%; Score 212; DB 2; Length 186485;
Matches 221; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 19 CCTAATCACCGATGTCACAGAGAGATCCAAAGAGAGGGCTCTTAGAGAGATGTA 78
Db 132476 CCTAATCACCGATGTCACAGAGATCCAAAGAGAGGGCTCTTAGAGAGATGTA 132417

Qy 79 AATCATCCTTGCTTGGAGACTGGACCCCTCACCGCTAACAGCAATTCAGGGATGGCTCT 138
Db 132416 AAATCATCCTTGCTTGGAGACTGGACCCCTCACCGCTAACAGCAATTCAGGGATGGCTCT 132357

Qy 139 TGTGTCTATAGAAATCTCTGGAGAGGAACAACAGCAATTCAGGGATGGCTCT 198
Db 132356 TGTGTCTATAGAAATCTCTGGAGAGGAACAACAGCAATTCAGGGATGGCTCT 132297

Qy 199 TGGGACATAGGGATGAGGACGCCATGTGAGTACGTCATGGCTCAATGCCGTCACT 254
Db 132296 TGGGACATAGGGATGAGGACGCCATGTGAGTACGTCATGGCTCAATGCCGTCACT 132241

RESULT 14			
ACI43769	ACI43769	160170 bp	DNA linear HTG 09-APR-2003
LOCUS	Macaca mulatta clone CH250-270D6	***	SEQUENCING IN PROGRESS ***.
DEFINITION	Macaca mulatta clone CH250-270D6		
ACCESSION	ACI43769		
VERSION	ACI43769.1		
KEYWORDS	HTGS PHASES; HTGS_PGI		
SOURCE	Macaca mulatta (<i>rhesus</i> -monkey)		
ORGANISM	Macaca mulatta		
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Cercopithecoidea; Cercopithecidae; Macaca.			
REFERENCE	1 (bases 1 to 160170)	*	
AUTHORS	Csuros, M. and Milosavljevic, A.	*	
TITLE	Pooled genomic indexing (PGI): mathematical analysis and experiment design	*	
JOURNAL	(11) Guigo, R. and Gusfield, D. (Eds.); ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI Springer (2002)	*	
REFERENCE	2 (bases 1 to 160170)	*	
AUTHORS	Milosavljevic, A., Sodergren, E., Csuros, M., Li, B., Jackson, A.R., Adams, C., Adio-Oduola, B., Al-Osman, F.R., Allen, C., Albrooks, S.L., Amarakunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbara, J., Bentzon, J., Blimke, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Briea, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J.J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Den, A.L., Ding, Y., Dinh, H., Douthwaite, R., Draper, H., Dugan-Rocha, S., Durbin, K.J., Egan, A., Earhart, C., Edwards, C.C., Elhai, J.C., Emerling, S., Escott, M., Falls, T., Ferragut, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabasi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Hawlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hooges, M., Hollaway, C., Hollins, B., Homsi, P., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karibian, E., Kelly, S., Khan, U., King, L., Korvan, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, J., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtenage, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozada, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Marcondel, I., Martin, R., Martindale, R., Martinez, E., Massay, E., Mawhinney, B., McLeod, M.P., Meador, M., Meli, G., Merscher, S., Metzker, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newson, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwolekwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payne, B., Perry, J., Perez, L., Peters, L., Pickens, R., Primus, E., Prol, L., Quiles, M., Ren, J., Rives, M., Rojas, A., Rojubolan, I., Rolfe, M., Ruiz, S., Saver, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shogbharti, N., Sisson, J., Sodergren, E., Sonnai, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamersaa, A., Tamersaa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vaquez, L., Vela, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczik, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.-F., Zhou, J., Zorrilla, S., Kucherlapati, R., Weinstock, G., and Gibbs, R.	*	
REFERENCE	3 (bases 1 to 160170)	*	
JOURNAL	Direct Submission	*	
REFERENCE		*	
AUTHORS	Worley, K.C.	*	
TITLE	Direct Submission	*	
JOURNAL	Submitted (10-APR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	*	
COMMENT	----- Genome Center	*	

RESULT 15			
ACI21264	ACI21264	194261 bp	DNA linear ROD 13 APR-2004
LOCUS	mus musculus chromosome 9, clone RP24-233P22, complete sequence		
DEFINITION	Mus musculus chromosome 9		
ACCESSION	ACI21264		
VERSION	ACI21264.8		
KEYWORDS	HTG		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.			
REFERENCE	1 (bases 1 to 194261)	*	

AUTHORS	Birren, B., Nusbaum, C. and Lander, E.
TITLE	Mus musculus chromosome 9, clone RP24-233F22
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 194261)
AUTHORS	Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Blodgett, T., Boukhalova, Y., Chazaro, B., Choepel, Y., Colangeli, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Pereira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K., Lamazares, R., Landers, T., Lehozcky, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., McDonnell, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Medin, J., Meineis, L., Mihowa, T., Mleenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Reelta, M., Rileback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rossetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talama, J., Testa, S., Theodore, J., Topham, K., Travers, M., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
REFERENCE	Submitted (16-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS	3 (bases 1 to 194261)
TITLE	Submitted (16-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
JOURNAL	Direct Submission
REFERENCE	3 (bases 1 to 194261)
AUTHORS	Birren, B., Nusbaum, C., Lander, E., Aboulela, I., Allen, N., Anderson, M., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgainer, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearlano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hapgood, D., Hedges, B., Hall, J., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C., Lindblad-Toh, K., Liu, X., Lui, A., Mabitt, R., Maclean, C., McDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melidrim, J., Meneus, L., Mleenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Reelta, M., Rileback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rossetti, M., Roy, A., Santos, R., Schauer, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talama, J., Testa, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
REFERENCE	4 (bases 1 to 194261)
AUTHORS	Birren, B., Nusbaum, C., Lander, E., Aboulela, I., Allen, N., Anderson, M., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgainer, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearlano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hapgood, D., Hall, J., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C., Lindblad-Toh, K., Liu, X., Lui, A., Mabitt, R., Maclean, C., McDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melidrim, J., Meneus, L., Mleenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Reelta, M., Rileback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rossetti, M., Roy, A., Santos, R., Schauer, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talama, J., Testa, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
REFERENCE	4 (bases 1 to 194261)
AUTHORS	Birren, B., Nusbaum, C., Lander, E., Aboulela, I., Allen, N., Anderson, M., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgainer, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearlano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hapgood, D., Hall, J., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C., Lindblad-Toh, K., Liu, X., Lui, A., Mabitt, R., Maclean, C., McDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melidrim, J., Meneus, L., Mleenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Reelta, M., Rileback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rossetti, M., Roy, A., Santos, R., Schauer, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talama, J., Testa, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

FEATURES	source
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COMMENT	Some of the sequence contained within base pairs 175167 to the end of the clone was stolen from accession AC108846 [WICGR Project L21006]. Location/Qualifiers
JOURNAL	Center code: WIBR Web site: http://www-beg.wi.mit.edu Contact: sequence_submissions@broad.mit.edu
REFERENCE	Center project name: L21224 Center clone name: 233_F_22

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Best Local Similarity 81.0%; Pred. No. 5e-40; Matches 47; Mismatches 0; Indels 0; Gaps 0;
Matches 200; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
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OY      259 TATGACA 265
Db      33450 GCTCACA 33456

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 Job time : 2231.25 secs

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GenCore version 5.1.6
 copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2005, 09:45:33 ; Search time 2037.02 Seconds
 (without alignment)

896.727 Million cell updates/sec

Title: US-09-996-630A-11_COPY_3800_4165

Perfect score: 366

Sequence: cccttaacctgtttcaaaa.....acatatttgttttagcaat 366

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Genbank:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sb:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	366	100.0	1641	AK026013
2	366	100.0	3361	AK025449
3	366	100.0	4165	AK025449
4	366	100.0	4882	HUMKIAQ
5	366	100.0	5140	BC071567
6	366	100.0	5519	AF226044
7	366	100.0	143034	AC104184
8	366	100.0	18685	AC138808
9	358	97.8	2580	G07259
10	300	82.0	396	AX337742
11	300	82.0	396	AX09056
12	149.6	40.9	252055	AC10612
13	132.2	36.1	4708	AF287809
14	132.2	36.1	162162	ALG72224
15	132.2	36.1	194261	AC121264
16	132.2	36.1	206641	AC120394
17	131.8	36.0	304	AX186951
18	120.8	33.0	329	AX185525
19	102.4	28.0	233777	AC100043

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
1	AK026013	Homo sapiens cDNA: FLJ22360 f19, clone HRC06511.	AK026013	1641 bp mRNA	linear	PRI 13-SEP-2003	
2	AK026013	Homo sapiens cDNA: FLJ22360 f19, clone HRC06511.	AK026013	1641 bp mRNA	linear	PRI 13-SEP-2003	
3	AK026013.1	GI_10438715					
4							
5							
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8							
9							
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12							
13							
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COMMENT

NEDO human cDNA sequencing project
 Unpublished

REFERENCE

1 Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikeda,Y., Nishi,T., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.

REFERENCE

1 NEDO human cDNA sequencing project

REFERENCE

2 (bases 1 to 1641)

AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.

TITLE Direct Submission

JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: fcdna@ims.u-tokyo.ac.jp), Tel: 81-3-5449-5286, Fax: 81-3-5449-5286

COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; 5' - 3' end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partially supported by Science and Technology Agency).

FEATURES source

1. -1641 /organism="Homo sapiens"
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 /clone="HRC06511"
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ORIGIN

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Db 1259 CCCCTAACCTGTCATCAAGTGCATAGTAGTGATAATTAAATTGTG 1318

Qy 61 GAAACACTCTGATTTCTGTATGGTATAATAAATGACTCTGGC 120
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Qy 121 AATTCATCTGTTAAAGTGACATCTGACCATTTAGAGTAGCTGAG 180
Db 1379 AATTCATCTGTTAAAGTGACATCTGACCATTTAGAGTAGCTGAG 1438

Qy 181 ACCGAATTAAGATAATCCCTACAACTGAAATGAGGTACAGAT 240
Db 1439 ACCGAATTAAGATAATCCCTACAACTGAAATGAGGTACAGAT 1498

Qy 241 TATCACTGTTGGTCAGTCCTCCAACTGCTGGTATTCCTCAATGCTAACAT 300
Db 1499 TATCACTGTTGGTCAGTCCTCCAACTGCTGGTATTCCTCAATGCTAACAT 1558

Qy 301 TGACAGGTGACAAATGGGAAAMAAATCCAAATAATAAGTGCAT 360
Db 1559 TGACAGGTGACAAATGGGAAAMAAATCCAAATAATAAGTGCAT 1618

Qy 361 AGCAAT 366
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Qy 61 GAAACACTCTGATTTCTGTATGGTATAATAAATGACTCTGGC 120
Db 3031 GAAAACACTCTGATTTCTGTATGGTATAATAAATGACTCTGGC 3090

Qy 181 ACCGAATTAAGATAATCCCTACAACTGAAATGAGGTACAGAT 240
Db 3151 ACCGAATTAAGATAATCCCTACAACTGAAATGAGGTACAGAT 3210

Qy 241 TATCACTGTTGGTCAGTCCTCCAACTGCTGGTATTCCTCAATGCTAACAT 300
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Qy 301 TGACAGGTGACAAATGGGAAAMAAATCCAAATAATAAGTGCAT 360
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RESULT 2

AK025449 AK025449 3361 bp mRNA linear PRI 13-SEP-2003

DEFINITION Homo sapiens cDNA: FLJ21796 fis, clone HEPP00537.

ACCESSION AK025449
VERSION AK025449.1
KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 GR:10437966
AUTHORS Bukayrova; Metzoco; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 GR:449.1
AUTHORS Okamoto,S., Hikiji,T., Kobatake,N., Inagaki,H., Ikeda,Y., Ohayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.

TITLE Unpublished
JOURNAL (bases 1 to 3361)
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.

TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirakane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: fcdna@ims.u-tokyo.ac.jp), Tel: +81-3-5449-5286, Fax: +81-3-5449-5416

COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' - & 3' -end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency). Location/Qualifiers

FEATURES source
ORIGIN
Query Match 100.0%; Score 366; DB 6; Length 4165;
Best Local Similarity 100.0%; Pred. No. 1.4e-64; Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1. .3361

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/mol_type="mRNA"

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RRDSSCRRPGEGDGGSGOSKUSNASGVDURKSPSENAGSGPSSEGGNTNTSGT
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Db 4100 TGACAGGTATGTGACAATGGGAAAAAATCCAAATAATAAAGTGACATATGGTGC 4159 ORIGIN

QY 361 AGCAT 366 Query Match 100%; Score 366; DB 9; Length 4882;
Db 4160 AGCAT 4165 Best Local Similarity 100%; Pred. No. 1 4e-64;
Matches 366; Conservative 0; Mismatched 0; Indels 0; Gaps 0;

RESULT 4

HUMKIAAQ LOCUS HUMKIAAQ 4982 bp mRNA for KIAA0096 gene, partial cds. linear PRI 10-MAY-2002
DEFINITION Human mRNA for KIAA0096 gene, partial cds.
ACCESSION D43636
VERSION D43636.2 GI:20521877
KEYWORDS KIAA0096
SOURCE Homo sapiens (human)
ORGANISM Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi;
REFERENCE Nagase,T., Miyata,N., Tanaka,A., Sazuka,T., Seki,N., Sato,S.,
AUTHORS Tabata,S., Irahima,K.-i., Kawarabayashi,Y., Kotani,H. and Nomura,N.
TITLE Prediction of the coding sequences of unidentified human genes.
III. The coding sequences of 40 new genes (KIAA0081-KIAA0120)
reduced by analysis of cDNA clones from human cell line KG-1
JOURNAL DNA Res. 2, 111-1743 (1995)
MEDLINE 95308325
PUBMED 7788527
REFERENCE Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
AUTHORS Submitted (24-NOV-1994) Osamu Ohara, Kazusa DNA Research Institute,
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:cdna@kazusa.or.jp, Tel:+81-438-52-3913)
COMMENT On May 9, 2002 this sequence veranion replaced gi:598957.
FEATURES source RESULT 4

1. 4882 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ha01240s1"
/sex="male"
/cell_line="KG-1"
/cell_type="myeloblast"
/tissue_type="brain"
/clone_Tib="Bluescript II SK plus"
/notes="This sequence was obtained by subcloning of the DNA
fragments derived from two cDNA clones (1 - 1013 was
derived from a RT-PCR product (lung) and 1014 - 4882 was
derived from ha01240)."
1. .4882
<!. .2302
<!. .genes="KIAA0096"
<!. .genes="KIAA0096"
/genes="KIAA0096" /notes="KIAA0096 gene product is related to a protein
kinase."

Db 4517 CCCTTAACCTGTCTCAAAGTGCAATAGTAGCTACAGTGATAAATTATCTG 50 Query Match 100%; Score 366; DB 9; Length 4882;
Db 4697 ACCGATTAAGATATCCCTACCAAGTGAATAGTGATGTTAGGGTACAGT 4756 Best Local Similarity 100%; Pred. No. 1 4e-64;
Matches 366; Conservative 0; Mismatched 0; Indels 0; Gaps 0;

Db 4577 GAAAACAGCTCTGTTTAAGATGAGTGAACTTAAAGATAGTG 180 Query Match 100%; Score 366; DB 9; Length 4882;
Db 4637 AATTCTATCTGTTTAAGATGAGTGAACTTAAAGATAGTG 4636 Best Local Similarity 100%; Pred. No. 1 4e-64;
Matches 366; Conservative 0; Mismatched 0; Indels 0; Gaps 0;

Db 4637 AATTCTATCTGTTTAAGATGAGTGAACTTAAAGATAGTG 4696 Query Match 100%; Score 366; DB 9; Length 4882;
Db 4697 ACCGATTAAGATATCCCTACCAAGTGAATAGTGATGTTAGGGTACAGT 4756 Best Local Similarity 100%; Pred. No. 1 4e-64;
Matches 366; Conservative 0; Mismatched 0; Indels 0; Gaps 0;

Db 4757 TACGACTATGGTCACTGCTTCATGCTGTTGATTCCTCTATGTTGAACT 300 Query Match 100%; Score 366; DB 9; Length 4882;
Db 4817 TGACAGGTATGTGACAATGGGAAAAAATCCAAATAATAAAGTGACATATGGTGC 4876 Best Local Similarity 100%; Pred. No. 1 4e-64;
Matches 366; Conservative 0; Mismatched 0; Indels 0; Gaps 0;

Db 4817 TGACAGGTATGTGACAATGGGAAAAAATCCAAATAATAAAGTGACATATGGTGC 4882 Query Match 100%; Score 366; DB 9; Length 4882;
Db 4882 AGCAT 4882 Best Local Similarity 100%; Pred. No. 1 4e-64;
Matches 366; Conservative 0; Mismatched 0; Indels 0; Gaps 0;

RESULT 5

LOCUS BC071567 5140 bp mRNA linear PRI 25-JUN-2004
DEFINITION Homo sapiens SNR-1 related kinase, mRNA (cDNA clone MGC:87067
IMAGE:4376623), complete cds.
ACCESSION BC071567
VERSION BC071567.1 GI:47939483
KEYWORDS MGC
SOURCE Homo sapiens (human)
ORGANISM Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi;
REFERENCE 1 (basea 1 to 5140)
AUTHORS Straubhaar,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G.,
Klauser,R.D., Collina,F.S., Wagner,L., Shemesh,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhattacharyya,
Hopkins,R.F., Jordon,H., Moore,T., Max,S.I., Wang,J.J., Heisler,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loqueline,N.A., Peters,G.J.,

REFERENCE
1 (bases 1 to 186485)
DOE Joint Genome Institute.
TITLE
Sequencing of Human Chromosome 5
JOURNAL
Unpublished

REFERENCE
2 (bases 1 to 186485)
DOE Joint Genome Institute.
TITLE
Direct Submission

COMMENT
Submitted (21JAN-2003) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Center: Joint Genome Center
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: RPCI-11-1026122
Center Clone Name: RPCI-11-1026122

Summary Statistics
Consensus quality: 182487 bases at least Q40
Consensus quality: 183346 bases at least Q30
Consensus quality: 183866 bases at least Q20
Estimated insert size: 17500; agarose-fp estimation
Estimated insert size: 186085; sum-of-contigs estimation
Quality coverage: 9.4 in Q20 bases; agarose-fp estimation
Quality coverage: 8.84 in Q20 bases; sum-of-contigs estimation.

NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1126: contig of 1126 bp in length
1127 1226: gap of unknown length
1227 2350: contig of 1124 bp in length
2351 2451 3522: 9bp of unknown length
3523 3622: contig of 1072 bp in length
3623 1173: contig of 7551 bp in length
1173 1174 1174: 9bp of unknown length
1174 186485: contig of 175212 bp in length.

FEATURES SOURCE
Location/Qualifiers
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/clone="RPL1-1026122"
/clone_lib="RPCI human BAC library 11"
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Query Mstch 100.0%; Score 366; DB 2; Length 186485;
Best Local Similarity 100.0%; Prod. No. 6.7e-65;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCCTAACCGTCTCAAGATGCTATGTTACAGTAGTGATAATTAAATTGCG 60
Db 121990 CCCTAACCGTCTCAAGATGCTATGTTACAGTAGTGATAATTAAATTGCG 121931
OY 61 GAAGAACAGCTGTGATTTCGTGTTATATATATGTACTCTGC 120
Db 121930 GAAGAACAGCTGTGATTTCGTGTTATATATATGTACTCTGC 121871
OY 121 ATTCATCTGTTAAGATGACAATCTGACCAATTAGATAGCTGTGAG 180
Db 121870 AATTCATCTGTTAAGATGACAATCTGACCAATTAGATAGCTGTGAG 121811
OY 181 ACCGATTAAGATAATCCCTACCAAGTGAATAATGATGTTAGAGGGTACAGAT 240
Db 121810 ACCGATTAAGATAATCCCTACCAAGTGAATAATGATGTTAGAGGGTACAGAT 121751

RESULT 9
G07259 G07259 2580 bp DNA linear STS 19-OCT-1995
LOCUS G07259 human STS WI-9354, sequence tagged site.
DEFINITION G07259 human STS WI-9354, sequence tagged site.
VERSION G07259.1 GI:890504
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Bureleostomi; Mammalia; Butcheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2580)
AUTHORS Hudson, T
TITLE Whitehead Institute/MIT Center for Genome Research; Physically Mapped ESTs
JOURNAL Unpublished (1995)
COMMENT
Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu
Primer A: GTGATTATGATAGCTTGGATGG
Primer B: AATGGTCACACTGCTGATCC
STS size: 121
PCR Profile:
Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
Protocol:
Template: 10 ng
Primer: each 5 pm
dNTPs: each 4 nm
Tag Polymerase: 0.025 units/ul
Total Vol: 20 ul
Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3
FEATURES SOURCE
Prepared with primer pairs derived from D43636 -- Unigene.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
(ab_xref="exon:9606"
/map="64_E_9; 792_D_7; 817_D_5; 882_B_5; 897_F_7;
946_E_4; 955_E_2; 738_F_11"
1871..1991
1871..1895
STS primer_bind
primer_bind complement(1971..1991)

ORIGIN

Query Match 97.8%; Score 358; DB 11; Length 2580;
 Best Local Similarity 97.8%; Pred. No. 6.5e-63; Matches 358; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CCCTTAACCTGCTTCAAAAGTCATAAGTACAGTAGTGATGTGTTAATTAATATGTG 60
 Db 2215 CCCCTAACCTGCTTCAAAAGTCATAAGTACAGTAGTGATGTGTTAATTAATATGTG 60
 Qy 61 GAAAACAGCTGTGATTTCGTGATGTGTTAATTAATATGTG 120
 Db 2275 GAAAACAGCTGTGATTTCGTGATGTGTTAATTAATATGTG 120
 Qy 121 AATTCATCTGTGTTAATAGATGACATGACATCTGACACCAATTAGAATAGCTGAG 180
 Db 2335 AATTCATCTGTGTTAATAGATGACATGACATCTGACACCAATTAGAATAGCTGAG 2394
 Qy 181 ACCGAATTAAGATAATCCCTACCAACTGAAATTGATGCTGTTAAGAGGGTACAGAT 240
 Db 2395 ACCGAATTAAGATAATCCCTACCAACTGAAATTGATGCTGTTAAGAGGGTACAGAT 2454
 Qy 241 TATCAACTGATTGGTCGTGTTCCATGCTGGTGTATTCCCTCATGGTAAACAT 300
 Db 255 TATCAACTGATTGGTCGTGTTCCATGCTGGTGTATTCCCTCATGGTAAACAT 2514
 Qy 301 TGACAGGTATGACAATGGAAAAAAATCCAATATAAAGTACATATTGGTGTIC 360
 Db 2515 TGACAGGTATGACAATGGAAAAAAATCCAATATAAAGTACATATTGGTGTIC 2574
 Qy 361 AGCAAT 366
 Db 2575 AGCAAT 2580

RESULT 10
 AX337742/c
 LOCUS AX337742 396 bp DNA linear PAT 09-JAN-2002
 DEFINITION Sequence 8251 from Patent WO0194629.
 ACCESSION AX337742
 VERSION AX337742.1 GI:18128461
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endreis, G., Horrigan, S., Soppe, D.R. and Weaver, Z.
 TITLE Cancer gene determination and therapeutic screening using signature gene sets
 JOURNAL Patent: WO 0194629-A 8251 13-DEC-2001;
 FEATURES source
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 /note="EMBL/GenBank Accession No. D60769"
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 Best Local Similarity 91.0%; Pred. No. 5.3e-51; Matches 333; Conservative 17; Mismatches 13; Indels 3; Gaps 3;

Qy 1 CCCTTAACCTGCTTCAAAAGTCATAAGTACAGTAGTGATGTGTTAATTAATATGTG 60
 Db 363 CCCCTAACCTGCTTCAAAAGTCATAAGTACAGTAGTGATGTGTTAATTAATATGTG 304
 Qy 61 GAAAACAGCTGTGATTTCGTGATGTGTTAATTAATATGTG 120
 Db 363 CCCCTAACCTGCTTCAAAAGTCATAAGTACAGTAGTGATGTGTTAATTAATATGTG 304
 Qy 61 GAAAACAGCTGTGATTTCGTGATGTGTTAATTAATATGTG 120
 Db 303 G-GAAACAGCTGTGATTTCGTGATGTGTTAATTAATATGTG 245
 Db 244 ADTCTAWCTGTAWTAAGATGTCRAACTCTGACHCRAATTAGATGCTGAG 185
 Qy 181 ACCGAATTAAGATAATCCCTACCAACTGAAATTGATGCTGTTAAGAGGGTACAGAT 240
 Db 184 ACCGRAT-AAGATAATCCCTACCAACTGAAATTGATGCTGTTAAGAGGGTACAGAT 126
 Qy 241 TATCAACTGATTGGTCGTGTTCCATGCTGGTGTATTCCCTCATGGTAAACAT 300
 Db 125 TATCAACTGATTGGTCGTGTTCCATGCTGGTGTATTCCCTCATGGTAAACAT 67
 Qy 301 TGACAGGTATGACAATGGAAAAAAATCCAATATAAAGTACATATTGGTGTIC 360
 Db 66 TGACAGGTATGACAATGGAAAAAAATCCAATATAAAGTACATATTGGTGTIC 7
 Qy 361 AGCAAT 366

ORIGIN
 Query Match 91.0%; Score 300; DB 6; Length 396;
 Best Local Similarity 91.0%; Pred. No. 5.3e-51; Matches 333; Conservative 17; Mismatches 13; Indels 3; Gaps 3;

Qy 1 CCCTTAACCTGCTTCAAAAGTCATAAGTACAGTAGTGATGTGTTAATTAATATGTG 60
 Db 244 ADTCTAWCTGTAWTAAGATGTCRAACTCTGACHCRAATTAGATGCTGAG 185
 Qy 181 ACCGAATTAAGATAATCCCTACCAACTGAAATTGATGCTGTTAAGAGGGTACAGAT 240
 Db 184 ACCGRAT-AAGATAATCCCTACCAACTGAAATTGATGCTGTTAAGAGGGTACAGAT 126
 Qy 241 TATCAACTGATTGGTCGTGTTCCATGCTGGTGTATTCCCTCATGGTAAACAT 300
 Db 125 TATCAACTGATTGGTCGTGTTCCATGCTGGTGTATTCCCTCATGGTAAACAT 67
 Qy 301 TGACAGGTATGACAATGGAAAAAAATCCAATATAAAGTACATATTGGTGTIC 360
 Db 66 TGACAGGTATGACAATGGAAAAAAATCCAATATAAAGTACATATTGGTGTIC 7
 Qy 361 AGCAAT 366

Db	6 AGCAT 1	REFERENCE AC106612/c DEFINITION Rattus norvegicus clone CH230-175A5, *** SEQUENCING IN PROGRESS ACCESSION AC106612 VERSION AC106612.5 KEYWORDS HTGS PHASE1; HTGS_DRAFT; HTGS_ENRICHED ORGANISM Rattus norvegicus (Norway rat) Rattus norvegicus (Norway rat)
REFERENCE AUTHORS	1 (bases 1 to 252055) Muzny,D., Metzker,M., Lee,, Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyabechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandarsnaskie,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,K., Blair,J., Blitskenberg,K., Blutch,P., Brown,M., Bryant,N., Buhan,C., Burch,P., Burrell,K., Calderon,B., Cerdenas,V., Carrer,K., Cesario,I., Ceaser,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., Di Souza,L., Devila,M.L., Davis,C., Davy-Csroll,I., De Andra,C., Dederich,D., Delgado,O., Denson,S., Demamo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Dual,B., Eaves,K., Egan,A., Ebdottom,M., Bugenhagen,C., Evans,C.A., Fallis,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gaojia,A., Ganta,R., Garcia,A., Game,T., Gaze,M., Gebridegoebis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Gunsritne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Hervay,Y., Havlik,P., Hsuesh,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hlaudin,S.L., Hodges,M., Hollins,B., Howell,S., Hulyk,S., Huime,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jollivet,A., Karpathy,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longsore,S., Lopez,J., Lorenshewa,L., Loulaged,H., Lozano,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Moshmoud,M., Mailly,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,T.Z., Martinez,E., McWhiney,S., McLeod,M.P., McNeil,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidas,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemech,O., Okwuonu,G., OlajumppaGoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,L., Pfannkoch,C., Plopper,F., Poinexter,A., Popovic,D., Primus,B., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richardson,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvastebeyn,A., Sison,I., Sittler,C.D., Smajs,D., Snied,A., Soedergren,E., Song,X.-Z., Sorelle,R., Soba,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Verbs,V., Vilissus,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Wilson,R., Wleczek,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakuob,S., Yen,J., Yoon,L., Yoon,W., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausen,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.	
REFERENCE AUTHORS	2 (bases 1 to 252055) Unpublished Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 252055) Rat Genome Sequencing Consortium Direct Submission	
REFERENCE TITLE JOURNAL REFERENCE AUTHORS	of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 252055) Rat Genome Sequencing Consortium Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 13, 2003 this sequence version replaced 91-24819088. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly ('a contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table. ----- Genome Center of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu ----- Project Information Center project name: GURO Center clone name: CH230-175A5 ----- Summary Statistics Assembly program: Atlab 3.0; Consensus quality: 216498 bases at least Q40 Consensus Quality: 220368 bases at least Q30 Consensus quality: 223168 bases at least Q20 Estimated insert size: 220938; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation ----- * NOTE: Estimated insert size may differ from sequence length * (see http://www.hgsc.bcm.tmc.edu/docs/Gebain_draft_data.html). * NOTE: This is a working draft sequence. It currently * consists of 6 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. * 243681: contig of 243681 bp in length * 243781: gap of unknown length * 243782: 244985: contig of 1204 bp in length * 244985: 245086: gap of unknown length * 245086: 246426: contig of 1341 bp in length * 246427: 246526: gap of unknown length * 246527: 247527: contig of 1001 bp in length * 247528: 247627: gap of unknown length * 247628: 248934: contig of 1307 bp in length * 248935: 249035: gap of unknown length * 249035: 250535: contig of 3021 bp in length. ----- FEATURES source organism=Rattus norvegicus" /mol_type="genomic DNA" /db_xref="taxon:10116" /clone="CH230-175A5" 1303..1905 /not_e="clone boundary clone_end:SP6 site:EcoRI ----- misc_feature end sequence:BH351404" /notes="clone_boundary clone_end:T7 site:EcoRI	

us-09-996-630a-11 copy 3800 4165.rges

JOURNAL Submitted (28-AUG-2002) Wellcome Trust Sanger Institute, Hinxton
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquer@sanger.ac.uk Clone requests: clonesrequest@sanger.ac.uk
On Aug 30, 2002 this sequence version replaced gi:22415879.
COMMENT

Center: Wellcome Trust Sanger Institute
Center code: SC

Contact: humquery@aanger.ac.uk

During sequence assembly data is where differences are found these together with a note of the number

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL:, Sw:, SWISSPROT:, Tr:, TRIMBL:, Wp:, WORMPEP;. Information on the WORMPEP database can be found at:
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-360E14 is from the RPCI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: PBAC3.6.
location: malfiers

source
1. .162162
Organism="Mus musculus"

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'clone="RP23-360B14"  
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RESULT 15
AC121264

Submitted (16-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 134261)
 Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Boguslavsky, L., Boukhalter, B., Comarck, J., Chang, J., Choepl, Y., Collymore, A., Cook, A., Cooke, P., Cormier, B., Delellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyne, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamt, A., Karatas, A., Kelts, C., Lander, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., McDonald, P., Major, J., Manning, J., Matchewa, C., McCarthy, M., Meldej, J., Menas, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguen, C., Nicol, R., North, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunichang, P., Pierre, N., Rachupka, A., Ramamurthy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Stubbs, M., Talama, J., Tsfay, S., Theodore, J., Topham, K., Travers, M., Vassilieff, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (11-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 19461)
 Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Archibald, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Comarck, J., Chang, J., Choeppl, Y., Collymore, A., Cook, A., Cooke, P., Cormier, B., Delellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyne, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamt, A., Karatas, A., Kelts, C., Lander, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., McDonald, P., Major, J., Manning, J., Matchewa, C., McCarthy, M., Meldej, J., Menas, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguen, C., Nicol, R., North, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunichang, P., Pierre, N., Rachupka, A., Ramamurthy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Stubbs, M., Talama, J., Tsfay, S., Theodore, J., Topham, K., Travers, M., Vassilieff, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (11-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 19461)
 Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Archibald, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Comarck, J., Chang, J., Choeppl, Y., Collymore, A., Cook, A., Cooke, P., Cormier, B., Delellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyne, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamt, A., Karatas, A., Kelts, C., Lander, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., McDonald, P., Major, J., Manning, J., Matchewa, C., McCarthy, M., Meldej, J., Menas, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguen, C., Nicol, R., North, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunichang, P., Pierre, N., Rachupka, A., Ramamurthy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Stubbs, M., Talama, J., Tsfay, S., Theodore, J., Topham, K., Travers, M., Vassilieff, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (11-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,
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 Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,
 Zimmer, A., and Zody, M.
 Direct Submission
 JOURNAL
 Submitted (13-APR-2004) Whitehead Institute/MIT Center for Genome Research, 3200 Charles Street, Cambridge, MA 02141, USA
 On Apr 13, 2004 this sequence version replaced gi:45356220.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Project Information
 Center Project name: L21224
 Center Clone name: 233_F_22

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Tue Feb 1 09:08:45 2005

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Page 13

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Search completed: January 31, 2005, 16:38:39
Job time : 2043.02 secs

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OM nucleic - nucleic search, using bw model

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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LOCUS	AX743697	
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VERSION	AX743697.1	PAT 14-MAY-2003
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ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
REFERENCE	Yue.H., Tang, Y.T., Nguyen,D.B., Yao,M.G., Xu,Y., Tribouley,C.M., Sanjanwala,M.S., Malia,N.K., Baughn,M.R., Sepperstein,S.K., Lal,P., Thornton,M., Gandhi,A.R., Ramkumar,J.J., Elliott,V.S., Arvizu,C., Thampavelu,K., Gietzen,K.J., Ding,L., Au-Young,J., Tran,B., Polley,J.L., Lee,S., Liu,D.A.M., Burford,N., Warren,B.A., Gururajan,R., Duggan,B.M., Honchell,C.D. and Hafalia,A.J.A.	
AUTHORS		
TITLE	Secreted human proteins	
JOURNAL	Patent: WO 0226982 A	
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5	388	100.0	4187	6	BD26417	BD26417 Sequence
6	388	100.0	4187	6	AX026417	AX026417 Sequence
7	388	100.0	4187	6	AX409692	AX409692 Sequence
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DEFINITION	Methods of diagnosing or treating neurological diseases and cell degeneration.						
ACCESSION	BD272343						
VERSION	BD272343.1						
KEYWORDS	JP 2002510076-A/3.						
SOURCE	Homo sapiens (human)						
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
AUTHORS	Nitsch, R. and Greeve, I.						
TITLE	Methods of diagnosing or treating neurological diseases and cell degeneration						
JOURNAL	Patent: JP 2002510076-A 3 17-SEP-2002;						
COMMENT	OS Homo sapiens (human)						
PN	JP 2002510076-A/3						
PD	17-SEP-2002						
PP	12-NOV-1999	JP 2000582553					
PR	12-NOV-1998	EP 98121478-6					
PI	ROGER NITSCH, ISABEL GREEVE						
PC	C12N15/09, A61K39/395, A61K39/395, A61K45/00, A61K49/00,						
PC	A61P1/00, A61P15/00, A61P21/00, A61P25/00, A61P25/14, A61P25/16, A61P25/28,						
PC	A61P43/00, C07K14/47, C07K16/19, C12N1/19, C12N1/21, C12N5/10, C12Q1/68, G01N33/53, G01N33/53, C12N15/00, C12N5/00, A61K39/702 CC						
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CC	degeneracion						
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DEFINITION							
ACCESSION	AX026418						
VERSION	AX026418.1						
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REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
AUTHORS	1 Nitsch, Roger M PROF DR DE						
TITLE	Methods of diagnosing or treating neurological diseases						
JOURNAL	Patent: EP 1002862-A 4 24-MAY-2000;						
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ACCESSION AX334630
VERSION AX334630.1 GI:18125349
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiensB
REFERENCE 1 Young, P.E., Augustus M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppe, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature gene sets
JOURNAL Patent: WO 0194629-A 5 139 13-DEC-2001;
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AX408962
LOCUS AX408962
DEFINITION Sequence 1609 from Patent WO0229103.
VERSION AX408962.1 GI:21441667
KEYWORDS
REFERENCE 1 Al-Mahmood, S., Colin, S. and Schneider, C.
TITLE Genes involved in regulating angiogenesis, pharmaceutical preparations containing same and applications thereof
JOURNAL Patent: WO 03074073-A 53 12-SEP-2003;
FEATURES source
1. .4187 /organism="Homo sapiens"
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 DEFINITION D13643.2 GI:6630631
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 SOURCE Homo sapiens (human)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Nomura,N., Miyajima,N., Suzuki,T., Tanaka,A., Kawarabayasi,Y.,
 Sato,S., Nagase,T., Seki,N., Ishikawa,K. and Tabata,S.
 TITLE Prediction of the coding sequences of unidentified human genes. I.
 The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
 analysis of randomly sampled cDNA clones from human immature
 myeloid cell line KG-1
 JOURNAL DNA Res. 1 (1), 27-35 (1994)
 MEDLINE 96051387
 PUBMED 7584026
 REFERENCE 2
 AUTHORS Nomura,N., Miyajima,N., Suzuki,T., Tanaka,A., Kawarabayasi,Y.,
 Sato,S., Nagase,T., Seki,N., Ishikawa,K. and Tabata,S.
 TITLE Prediction of the coding sequences of unidentified human genes. I.
 The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
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 myeloid cell line KG-1 (supplement)
 JOURNAL DNA Res. 1 (1), 47-56 (1994)
 MEDLINE 96051389
 PUBLMED 7584028
 REFERENCE 3 (bases 1 to 4187)
 AUTHORS Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
 TITLE Direct Submission
 JOURNAL Submitted (11-NOV-1992) Oamu Ohara, Kazusa DNA Research Institute;
 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
 COMMENT On Dec 22, 1999 this sequence version replaced gi:288996.
 Sequence updated (20-Dec-1999).

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 VERSION MGC.4
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 AUTHORS 1 (bases 1 to 4202)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shemesh, C.M., Schulier, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J.J., Hsieh, P.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

REFERENCE 1
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Stapleton, M., Soares, M.B., Bonaldo, M.F., Cesavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carrinici, P., Prange, C., Raha, S.S., Loqueline, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., Mcowan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Farhey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J.J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smialius, E., Scherich, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 4202)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC); Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncbi.nih.gov>
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: ARCC
DNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Jiao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anna Petrescu, Anna Lisa Prahar, Parvaneh Saeedi, JR Santos, Angelique Scherich, Ursula Skalska, Duane Smilus, Jeff Stott, Miranda Tsai, George Yang, Jacqueline Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium@LLNL at: <http://image.llnl.gov>
Series: IRL1 Plate: 13 Row: f Column: 10.
FEATURES
source

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COMMENT
JOURNAL ROGER NITSCH, ISABEL GREBE
OS Homo sapiens (human)
COMMENT JP 2002/30076-A/1
ORGANISM Homo sapiens (human)
DBDEFINITION Methods of diagnosing or treating neurological diseases and cell degeneration.
ACCESSION BD272341
VERSION BD272341.1 GI:33082109
KEYWORDS SOURCE
REFERENCE BD272341
AUTHORS JP 2002/30076-A/1.
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AUTHORS JP 2002/30076-A/1.
TITLE Methods of diagnosing or treating neurological diseases and cell degeneration.
Patent: JP 2002/30076-A 1 17-SEP-2002,
ROGER NITSCH, ISABEL GREBE
OS Homo sapiens (human)
COMMENT JP 2002/30076-A/1
ORGANISM Homo sapiens (human)
DBDEFINITION Methods of diagnosing or treating neurological diseases and cell degeneration.
ACCESSION BD272341
VERSION BD272341.1 GI:33082109
KEYWORDS SOURCE
REFERENCE BD272341
AUTHORS JP 2002/30076-A/1.
TITLE Methods of diagnosing or treating neurological diseases and cell degeneration.
Patent: JP 2002/30076-A 1 17-SEP-2002,
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COMMENT JP 2002/30076-A/1
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OS Homo sapiens (human)
COMMENT JP 2002/30076-A/1
ORGANISM Homo sapiens (human)
DBDEFINITION Methods of diagnosing or treating neurological diseases and cell degeneration.
ACCESSION BD272341
VERSION BD272341.1 GI:33082109
KEYWORDS SOURCE
REFERENCE BD272341
AUTHORS JP 200

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 KEYWORDS SOURCE Homo sapiens (human)
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 REFERENCE 1 AUTHORS TITLE JOURNAL
 Methods of diagnosing or treating neurological diseases
 Patent: EP 1002862-A 2 24-MAY-2000;
 NITSCH ROGER M PROF DR (DE) Location/Qualifiers
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 DEFINITION linear PAT 12-DEC-2003

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 VERSION AX828386.1 GI:39838386
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 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 REFERENCE 1
 Al-Wahmood,S., Colin,S. and Schnieder,C.
 Genes involved in regulating angiogenesis, pharmaceutical
 preparations containing same and applications thereof
 Patent: WO 03074073-A 32 12-SEP-2003;
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 QY 361 TGCTCTGTTAATAAAGTGGCTGG 388
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Search completed: January 31, 2005, 16:38:28
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AUTHORS	Alvarez, C., Horne, D., Peres-Silva, S. and Vockley, J.G.	1	Best Local Similarity 100.0%; P-req. No. 1-8e-67;
TITLE	Gene expression profiles in liver cancer	0	Mismatches 0; Indels 0; Gaps 0;
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DEFINITION	Sequence 53 from Patent WO03074073.	DNA	linear
VERSION	AX028407.1	PAT	12-DEC-2003
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SOURCE	KIAA0018 protein.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Nomura, N., Miyajima, N., Suzuki, T., Tanaka, A., Kawarabayasi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S.		
AUTHORS	The prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA001-KIAA040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1		
JOURNAL	Nomura, N., Miyajima, N., Suzuki, T., Tanaka, A., Kawarabayasi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S.		
MEDLINE	0		
PUBLISHED	96051387		
REFERENCE	2		
AUTHORS	Nomura, N., Miyajima, N., Suzuki, T., Tanaka, A., Kawarabayasi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S.		
JOURNAL	0		
MEDLINE	96051387		
REFERENCE	3		
AUTHORS	Ohara, O., Nagase, T., Kikuno, R. and Nomura, N.		
JOURNAL	Submitted (11-Nov-1992) Ohara, Kazuya DNA Research Institute; 152-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp Tel:+81-43-3913)		
COMMENT	On Dec 22, 1999 this sequence version replaced gi:285996. Sequence updated (20-Dec-1999).		
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source	1. .4187 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"		

Tue Feb 1 09:08:40 2005

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Page 9

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